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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/078,059DATE: 03/05/2002 P.5  
TIME: 14:12:03Input Set : A:\PF466P2SEQLIST01102002.txt  
Output Set: N:\CRF3\03052002\J078059.raw

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3 <110> APPLICANT: Ruben et al.
5 <120> TITLE OF INVENTION: Cytokine Receptor Common Gamma Chain Like
7 <130> FILE REFERENCE: PF466P2
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/078,059
C--> 9 <141> CURRENT FILING DATE: 2002-02-20
9 <150> PRIOR APPLICATION NUMBER: 60/269,876
10 <151> PRIOR FILING DATE: 2001-02-21
12 <150> PRIOR APPLICATION NUMBER: PCT/US00/22493
13 <151> PRIOR FILING DATE: 2000-08-17
15 <150> PRIOR APPLICATION NUMBER: 09/376,430
16 <151> PRIOR FILING DATE: 1999-08-18
18 <150> PRIOR APPLICATION NUMBER: 09/263,626
19 <151> PRIOR FILING DATE: 1999-03-05
21 <150> PRIOR APPLICATION NUMBER: PCT/US99/05068
22 <151> PRIOR FILING DATE: 1999-03-05
24 <150> PRIOR APPLICATION NUMBER: 60/086,505
25 <151> PRIOR FILING DATE: 1998-05-22
27 <150> PRIOR APPLICATION NUMBER: 60/078,563
28 <151> PRIOR FILING DATE: 1998-03-19
30 <160> NUMBER OF SEQ ID NOS: 32
32 <170> SOFTWARE: PatentIn Ver. 2.1
34 <210> SEQ ID NO: 1
35 <211> LENGTH: 1573
36 <212> TYPE: DNA
37 <213> ORGANISM: Homo sapiens
39 <220> FEATURE:
40 <221> NAME/KEY: CDS
41 <222> LOCATION: (13)..(1125)
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46           1                     5                     10
48 ctg ctg gga ggc tgg atg gct ttg ggg caa gga gga gca gca gaa gga   99
49 Leu Leu Gly Gly Trp Met Ala Leu Gly Gln Gly Gly Ala Ala Glu Gly
50   15                     20                     25
52 gta cag att cag atc atc tac ttc aat tta gaa acc gtg cag gtg aca   147
53 Val Gln Ile Gln Ile Ile Tyr Phe Asn Leu Glu Thr Val Gln Val Thr
54 30                     35                     40                     45
56 tgg aat gcc agc aaa tac tcc agg acc aac ctg act ttc cac tac aga   195
57 Trp Asn Ala Ser Lys Tyr Ser Arg Thr Asn Leu Thr Phe His Tyr Arg
58           50                     55                     60
60 ttc aac ggt gat gag gcc tat gac cag tgc acc aac tac ctt ctc cag   243
61 Phe Asn Gly Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln

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62          65          70          75
64 gaa ggt cac act tcg ggg tgc ctc cta gac gca gag cag cga gac gac 291
65 Glu Gly His Thr Ser Gly Cys Leu Leu Asp Ala Glu Gln Arg Asp Asp
66          80          85          90
68 att ctc tat ttc tcc atc agg aat ggg acg cac ccc gtt ttc acc gca 339
69 Ile Leu Tyr Phe Ser Ile Arg Asn Gly Thr His Pro Val Phe Thr Ala
70          95          100          105
72 agt cgc tgg atg gtt tat tac ctg aaa ccc agt tcc ccg aag cac gtg 387
73 Ser Arg Trp Met Val Tyr Tyr Leu Lys Pro Ser Ser Pro Lys His Val
74 110          115          120          125
76 aga ttt tcg tgg cat cag gat gca gtg acg gtg acg tgt tct gac ctg 435
77 Arg Phe Ser Trp His Gln Asp Ala Val Thr Val Thr Cys Ser Asp Leu
78          130          135          140
80 tcc tac ggg gat ctc ctc tat gag gtt cag tac cgg agc ccc ttc gac 483
81 Ser Tyr Gly Asp Leu Leu Tyr Glu Val Gln Tyr Arg Ser Pro Phe Asp
82          145          150          155
84 acc gag tgg cag tcc aaa cag gaa aat acc tgc aac gtc acc ata gaa 531
85 Thr Glu Trp Gln Ser Lys Gln Glu Asn Thr Cys Asn Val Thr Ile Glu
86          160          165          170
88 ggc ttg gat gcc gag aag tgt tac tct ttc tgg gtc agg gtg aag gct 579
89 Gly Leu Asp Ala Glu Lys Cys Tyr Ser Phe Trp Val Arg Val Lys Ala
90          175          180          185
92 atg gag gat gta tat ggg cca gac aca tac cca agc gac tgg tca gag 627
93 Met Glu Asp Val Tyr Gly Pro Asp Thr Tyr Pro Ser Asp Trp Ser Glu
94 190          195          200          205
96 gtg aca tgc tgg cag aga ggc gag att cgg gat gcc tgt gca gag aca 675
97 Val Thr Cys Trp Gln Arg Gly Glu Ile Arg Asp Ala Cys Ala Glu Thr
98          210          215          220
100 cca acg cct ccc aaa cca aag ctg tcc aaa ttt att tta att tcc agc 723
101 Pro Thr Pro Pro Lys Pro Lys Leu Ser Lys Phe Ile Leu Ile Ser Ser
102          225          230          235
104 ctg gcc atc ctt ctg atg gtg tct ctc ctc ctt ctg tct tta tgg aaa 771
105 Leu Ala Ile Leu Leu Met Val Ser Leu Leu Leu Leu Ser Leu Trp Lys
106          240          245          250
108 tta tgg aga gtg aag aag ttt ctc att ccc agc gtg cca gac ccg aaa 819
109 Leu Trp Arg Val Lys Lys Phe Leu Ile Pro Ser Val Pro Asp Pro Lys
110          255          260          265
112 tcc atc ttc ccc ggg ctc ttt gag ata cac caa ggg aac ttc cag gag 867
113 Ser Ile Phe Pro Gly Leu Phe Glu Ile His Gln Gly Asn Phe Gln Glu
114 270          275          280          285
116 tgg atc aca gac acc cag aac gtg gcc cac ctc cac aag atg gca ggt 915
117 Trp Ile Thr Asp Thr Gln Asn Val Ala His Leu His Lys Met Ala Gly
118          290          295          300
120 gca gag caa gaa agt ggc ccc gag gag ccc ctg gta gtc cag ttg gcc 963
121 Ala Glu Gln Glu Ser Gly Pro Glu Glu Pro Leu Val Val Gln Leu Ala
122          305          310          315
124 aag act gaa gcc gag tct ccc agg atg ctg gac cca cag acc gag gag 1011
125 Lys Thr Glu Ala Glu Ser Pro Arg Met Leu Asp Pro Gln Thr Glu Glu
126          320          325          330

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128 aaa gag gcc tct ggg gga tcc ctc cag ctt ccc cac cag ccc ctc caa 1059
129 Lys Glu Ala Ser Gly Gly Ser Leu Gln Leu Pro His Gln Pro Leu Gln
130 335 340 345
132 ggc ggt gat gtg gtc aca atc ggg ggc ttc acc ttt gtg atg aat gac 1107
133 Gly Gly Asp Val Val Thr Ile Gly Gly Phe Thr Phe Val Met Asn Asp
134 350 355 360 365
136 cgc tcc tac gtg gcg ttg tgatggacac accactgtca aagtcaacgt 1155
137 Arg Ser Tyr Val Ala Leu
138 370
140 caggatcoac gttgacattt aaagacagag gggactgtcc cggggactcc acaccacccat 1215
142 ggatgggaag tctccacgcc aatgatggta ggactaggag actctgaaga ccagacctca 1275
144 ccgcctaattg cggccactgc cctgctaact ttccccaca tgagtctctg tgttcaaagg 1335
146 cttgatggca gatgggagcc aattgctcca ggagatttac tcccagttcc ttttcgtgcc 1395
148 tgaacgttgt cacataaacc ccaaggcagc acgtccaaaa tgctgtaaaa ccatcttccc 1455
150 actctgtgag tcccagttc cgtccatgta cctgttccat agcattggat tctcggagga 1515
152 tttttgtct gttttgagac tccaaaccac ctctaccctt aaaaaaaaaa aaaaaaaa 1573
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156 <211> LENGTH: 371
157 <212> TYPE: PRT
158 <213> ORGANISM: Homo sapiens
160 <400> SEQUENCE: 2
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162 1 5 10 15
164 Gly Trp Met Ala Leu Gly Gln Gly Gly Ala Ala Glu Gly Val Gln Ile
165 20 25 30
167 Gln Ile Ile Tyr Phe Asn Leu Glu Thr Val Gln Val Thr Trp Asn Ala
168 35 40 45
170 Ser Lys Tyr Ser Arg Thr Asn Leu Thr Phe His Tyr Arg Phe Asn Gly
171 50 55 60
173 Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln Glu Gly His
174 65 70 75 80
176 Thr Ser Gly Cys Leu Leu Asp Ala Glu Gln Arg Asp Asp Ile Leu Tyr
177 85 90 95
179 Phe Ser Ile Arg Asn Gly Thr His Pro Val Phe Thr Ala Ser Arg Trp
180 100 105 110
182 Met Val Tyr Tyr Leu Lys Pro Ser Ser Pro Lys His Val Arg Phe Ser
183 115 120 125
185 Trp His Gln Asp Ala Val Thr Val Thr Cys Ser Asp Leu Ser Tyr Gly
186 130 135 140
188 Asp Leu Leu Tyr Glu Val Gln Tyr Arg Ser Pro Phe Asp Thr Glu Trp
189 145 150 155 160
191 Gln Ser Lys Gln Glu Asn Thr Cys Asn Val Thr Ile Glu Gly Leu Asp
192 165 170 175
194 Ala Glu Lys Cys Tyr Ser Phe Trp Val Arg Val Lys Ala Met Glu Asp
195 180 185 190
197 Val Tyr Gly Pro Asp Thr Tyr Pro Ser Asp Trp Ser Glu Val Thr Cys
198 195 200 205
200 Trp Gln Arg Gly Glu Ile Arg Asp Ala Cys Ala Glu Thr Pro Thr Pro
201 210 215 220

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203 Pro Lys Pro Lys Leu Ser Lys Phe Ile Leu Ile Ser Ser Leu Ala Ile
204 225                230                235                240
206 Leu Leu Met Val Ser Leu Leu Leu Leu Ser Leu Trp Lys Leu Trp Arg
207                245                250                255
209 Val Lys Lys Phe Leu Ile Pro Ser Val Pro Asp Pro Lys Ser Ile Phe
210                260                265                270
212 Pro Gly Leu Phe Glu Ile His Gln Gly Asn Phe Gln Glu Trp Ile Thr
213                275                280                285
215 Asp Thr Gln Asn Val Ala His Leu His Lys Met Ala Gly Ala Glu Gln
216                290                295                300
218 Glu Ser Gly Pro Glu Glu Pro Leu Val Val Gln Leu Ala Lys Thr Glu
219 305                310                315                320
221 Ala Glu Ser Pro Arg Met Leu Asp Pro Gln Thr Glu Glu Lys Glu Ala
222                325                330                335
224 Ser Gly Gly Ser Leu Gln Leu Pro His Gln Pro Leu Gln Gly Gly Asp
225                340                345                350
227 Val Val Thr Ile Gly Gly Phe Thr Phe Val Met Asn Asp Arg Ser Tyr
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230 Val Ala Leu
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236 <211> LENGTH: 379
237 <212> TYPE: PRT
238 <213> ORGANISM: Homo sapiens
240 <400> SEQUENCE: 3
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245                20                25                30
247 Asn Glu Asp Ile Gly Gly Lys Pro Gly Thr Gly Gly Asp Phe Phe Leu
248                35                40                45
250 Thr Ser Thr Pro Ala Gly Thr Leu Asp Val Ser Thr Leu Pro Leu Pro
251                50                55                60
253 Lys Val Gln Cys Phe Val Phe Asn Val Glu Tyr Met Asn Cys Thr Trp
254 65                70                75                80
256 Asn Ser Ser Ser Glu Pro Gln Pro Asn Asn Leu Thr Leu His Tyr Gly
257                85                90                95
259 Tyr Arg Asn Phe Asn Gly Asp Asp Lys Leu Gln Glu Cys Gly His Tyr
260                100               105               110
262 Leu Phe Ser Glu Gly Ile Thr Ser Gly Cys Trp Phe Gly Lys Lys Glu
263                115               120               125
265 Ile Arg Leu Tyr Glu Thr Phe Val Val Gln Leu Gln Asp Pro Arg Glu
266                130               135               140
268 His Arg Lys Gln Pro Lys Gln Met Leu Lys Leu Gln Asp Leu Val Ile
269 145               150               155               160
271 Pro Trp Ala Pro Glu Asn Leu Thr Leu Arg Asn Leu Ser Glu Phe Gln
272                165               170               175
274 Leu Glu Leu Ser Trp Ser Asn Arg Tyr Leu Asp His Cys Leu Glu His
275                180               185               190

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277 Leu Val Gln Tyr Arg Ser Asp Arg Asp Arg Ser Trp Thr Glu Gln Ser
278           195                200                205
280 Val Asp His Arg His Ser Phe Ser Leu Pro Ser Val Asp Ala Gln Lys
281       210                215                220
283 Leu Tyr Thr Phe Arg Val Arg Ser Arg Tyr Asn Pro Leu Cys Gly Ser
284 225                230                235                240
286 Ala Gln His Trp Ser Asp Trp Ser Tyr Pro Ile His Trp Gly Ser Asn
287           245                250                255
289 Thr Ser Lys Glu Asn Ile Glu Asn Pro Glu Asn Pro Ser Leu Phe Ala
290           260                265                270
292 Leu Glu Ala Val Leu Ile Pro Leu Gly Ser Met Gly Leu Ile Val Ser
293       275                280                285
295 Leu Ile Cys Val Tyr Cys Trp Leu Glu Arg Thr Met Pro Arg Ile Pro
296       290                295                300
298 Thr Leu Lys Asn Leu Glu Asp Leu Val Thr Glu Tyr Gln Gly Asn Phe
299 305                310                315                320
301 Ser Ala Trp Ser Gly Val Ser Lys Gly Leu Ala Glu Ser Leu Gln Pro
302           325                330                335
304 Asp Tyr Ser Glu Arg Leu Cys His Val Ser Glu Ile Pro Pro Lys Gly
305           340                345                350
307 Gly Glu Gly Pro Gly Gly Ser Pro Cys Ser Gln His Ser Pro Tyr Trp
308           355                360                365
310 Ala Pro Pro Cys Tyr Thr Leu Lys Pro Glu Pro
311       370                375
314 <210> SEQ ID NO: 4
315 <211> LENGTH: 733
316 <212> TYPE: DNA
317 <213> ORGANISM: Homo sapiens
319 <400> SEQUENCE: 4
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321 aattcgaggg tgcaccgtca gtcttcctct tcccccaaaa acccaaggac accctcatga 120
322 tctcccgac tcctgaggtc acatgcgtgg tgggtggacgt aagccacgaa gaccctgagg 180
323 tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240
324 aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300
325 ggctgaatgg caaggagtac aagtgcgaag tctccaacaa agccctccca acccccatcg 360
326 agaaaacat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420
327 catcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaaggcttct 480
328 atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga 540
329 ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag ctcaccgtgg 600
330 acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggtctctg 660
331 acaaccacta cagcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc 720
332 gactctagag gat 733
335 <210> SEQ ID NO: 5
336 <211> LENGTH: 5
337 <212> TYPE: PRT
338 <213> ORGANISM: Homo sapiens
340 <220> FEATURE:
341 <221> NAME/KEY: SITE
342 <222> LOCATION: (3)

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/078,059

DATE: 03/05/2002

TIME: 14:12:04

Input Set : A:\PF466P2SEQLIST01102002.txt

Output Set: N:\CRF3\03052002\J078059.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:560 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18

L:580 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19

L:610 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20

L:625 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21

L:719 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25

L:722 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25

L:783 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26

L:835 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27

L:844 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27

L:894 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30